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STAZEWSKI, LENA
XU, HONG
EHEVERRI, FERNANDO

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<210> 6
<211> 852
<212> PRT
<213> Homo sapiens

<400> 6
Met Leu Gly Pro Ala Val Leu Gly Leu Ser Leu Trp Ala Leu Leu His
1 5 10 15

Pro Gly Thr Gly Ala Pro Leu Cys Leu Ser Gln Gln Leu Arg Met Lys

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Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
          35                  40                  45

Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
      50                  55                  60

Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
 65                  70                  75                  80

Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
                 85                  90                  95

Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
            100                 105                 110

Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
        115                 120                 125

Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
    130                 135                 140

His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
145                 150                 155                 160

Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala
                165                 170                 175

Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
            180                 185                 190

Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln Glu Phe Gly Trp Asn Trp
        195                 200                 205

Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr Gly Arg Gln Gly Leu Ser
    210                 215                 220

Ile Phe Ser Ala Leu Ala Ala Ala Arg Gly Ile Cys Ile Ala His Glu
225                 230                 235                 240

Gly Leu Val Pro Leu Pro Arg Ala Asp Asp Ser Arg Leu Gly Lys Val
                245                 250                 255

Gln Asp Val Leu His Gln Val Asn Gln Ser Ser Val Gln Val Val Leu
            260                 265                 270

Leu Phe Ala Ser Val His Ala Ala His Ala Leu Phe Asn Tyr Ser Ile
        275                 280                 285

Ser Ser Arg Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ala Trp Leu
    290                 295                 300

Thr Ser Asp Leu Val Met Gly Leu Pro Gly Met Ala Gln Met Gly Thr
305                 310                 315                 320

Val Leu Gly Phe Leu Gln Arg Gly Ala Gln Leu His Glu Phe Pro Gln
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                325                 330                 335

Tyr Val Lys Thr His Leu Ala Leu Ala Thr Asp Pro Ala Phe Cys Ser
            340                 345                 350

Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu Glu Asp Val Val Gly Gln
        355                 360                 365

Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu Gln Asn Val Ser Ala Gly
    370                 375                 380

Leu Asn His His Gln Thr Phe Ser Val Tyr Ala Ala Val Tyr Ser Val
385                 390                 395                 400

Ala Gln Ala Leu His Asn Thr Leu Gln Cys Asn Ala Ser Gly Cys Pro
                405                 410                 415

Ala Gln Asp Pro Val Lys Pro Trp Gln Leu Leu Glu Asn Met Tyr Asn
            420                 425                 430

Leu Thr Phe His Val Gly Gly Leu Pro Leu Arg Phe Asp Ser Ser Gly
        435                 440                 445

Asn Val Asp Met Glu Tyr Asp Leu Lys Leu Trp Val Trp Gln Gly Ser
    450                 455                 460

Val Pro Arg Leu His Asp Val Gly Arg Phe Asn Gly Ser Leu Arg Thr
465                 470                 475                 480

Glu Arg Leu Lys Ile Arg Trp His Thr Ser Asp Asn Gln Lys Pro Val
                485                 490                 495

Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys
            500                 505                 510

Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp Cys Glu Ala Gly Ser
        515                 520                 525

Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp
    530                 535                 540

Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg
545                 550                 555                 560

Phe Leu Ala Trp Gly Glu Pro Ala Val Leu Leu Leu Leu Leu Leu Leu
                565                 570                 575

Ser Leu Ala Leu Gly Leu Val Leu Ala Ala Leu Gly Leu Phe Val His
            580                 585                 590

His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys
        595                 600                 605

Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe
    610                 615                 620

Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser
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625 630 635 640

His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
645 650 655

Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
660 665 670

Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
675 680 685

Met Leu Val Glu Val Ala Leu Cys Thr Trp Tyr Leu Val Ala Phe Pro
690 695 700

Pro Glu Val Val Thr Asp Trp His Met Leu Pro Thr Glu Ala Leu Val
705 710 715 720

His Cys Arg Thr Arg Ser Trp Val Ser Phe Gly Leu Ala His Ala Thr
725 730 735

Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu Gly Thr Phe Leu Val Arg
740 745 750

Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg Gly Leu Thr Phe Ala Met
755 760 765

Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val Pro Leu Leu Ala Asn
770 775 780

Val Gln Val Val Leu Arg Pro Ala Val Gln Met Gly Ala Leu Leu Leu
785 790 795 800

Cys Val Leu Gly Ile Leu Ala Ala Phe His Leu Pro Arg Cys Tyr Leu
805 810 815

Leu Met Arg Gln Pro Gly Leu Asn Thr Pro Glu Phe Phe Leu Gly Gly
820 825 830

Gly Pro Gly Asp Ala Gln Gly Gln Asn Asp Gly Asn Thr Gly Asn Gln
835 840 845

Gly Lys His Glu
850

<210> 7
<211> 2559
<212> DNA
<213> Homo sapiens

<400> 7
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gtgtgcacca ggttctcctc aaacggcctg ctctgggcac tggccatgaa aatggccgtg 240
gaggagatca acaacaagtc ggatctgctg cccgggctgc gcctgggcta cgacctcttt 300
gatacgtgct cggagcctgt ggtggccatg aagcccagcc tcatgttcct ggccaaggca 360

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ctcatgcccc aggtcagcta cggtgctagc atggagctgc tgagcgcccg ggagaccttc 540
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<210> 8
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

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<221> MOD_RES
<222> (1)
<223> Thr or Arg

<220>
<221> MOD_RES
<222> (3)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (4)
<223> Arg, Gln or Pro

<220>
<221> MOD_RES
<222> (6)
<223> Arg or Thr

<220>
<221> MOD_RES
<222> (7)
<223> Ser, Pro or Val

<220>
<221> MOD_RES
<222> (8)
<223> Val, Glu, Arg, Lys or Thr

<220>
<221> MOD_RES
<222> (11)
<223> Ala or Glu

<220>
<221> MOD_RES
<222> (12)
<223> Trp or Leu

<220>
<221> MOD_RES
<222> (13)
<223> Arg, His or Gly

<400> 8
Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
1 5 10

<210> 9
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus sequence

<220>
<221> MOD_RES
<222> (1)
<223> Leu or Gln

<220>
<221> MOD_RES

<222> (3)
<223> Glu, Gly or Thr

<220>
<221> MOD_RES
<222> (4)
<223> Asn, Arg or Cys

<220>
<221> MOD_RES
<222> (7)
<223> Arg or Glu

<220>
<221> MOD_RES
<222> (9)
<223> Arg or Lys

<220>
<221> MOD_RES
<222> (10)
<223> Cys, Gly or Phe

<220>
<221> MOD_RES
<222> (11)
<223> Val, Leu or Ile

<220>
<221> MOD_RES
<222> (13)
<223> Phe or Leu

<220>
<221> MOD_RES
<222> (14)
<223> Ala or Ser

<220>
<221> MOD_RES
<222> (15)
<223> Met or Leu

<400> 9
Xaa Pro Xaa Xaa Tyr Asn Xaa Ala Xaa Xaa Xaa Thr Xaa Xaa Xaa
1 5 10 15

<210> 10
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 10
Ser Val Ser Thr Val Val
1 5